

**Veneration or violence: a Midwestern perspective of postmortem cultural modification of human bone.** SHIRLEY J. SCHERMER and ROBIN M. LILLIE, Office of the State Archaeologist, University of Iowa, Iowa City, IA 52242.

Examples of postmortem culturally modified bone appear in human skeletal remains in Iowa as early as the Late Archaic/Early Woodland and continue throughout the prehistoric period. The most prevalent form is cut marks. Other modifications include polishing, etching, drilling, cut-out rondels, burning, decapitation, and removal of the cranial base. At first glance, these modifications could suggest violence. However, upon closer evaluation other explanations are offered.

Detailed description, documentation, and skeletal patterning, evaluated within specific cultural contexts, suggest some of these modifications may relate to ceremonial burial processing or have protective or religious significance. The relationship to the deceased may then be seen as friendly or reverential rather than adversarial.

**Postmarital residence and population structure at Pueblo Bonito.** M.A. SCHILLACI and C.M. STOJANOWSKI, Department of Anthropology, University of New Mexico, NM 87131.

The great houses of Chaco Canyon form the core of a regional sociopolitical system integrating many communities within the San Juan Basin and surrounding areas of the American Southwest during the early PII and PIII periods (A.D. 1050-1140). Although this complexity has been the subject of considerable study, aspects of social organization such as postmarital residence have not received much attention. This paper examines Chacoan residence through an analysis of the skeletal samples collected during excavations at Pueblo Bonito by George Pepper (1890s) and Neil Judd (1920s).

We collected age and sex data, as well as data for 11 craniofacial variables, for the 27 individuals represented by these two samples. We investigated sex-specific pattern differences in variation using univariate F-tests and univariate Levene's tests. F-tests were then repeated on bootstrapped estimates of the variable standard deviations. We tested for multivariate variance differences using Van Valen's test. In addition, we calculated inter-individual Mahalanobis distances between all individuals and examined the pattern of relatedness within and between samples.

The results of this analysis do not support a hypothesis of matrilocality for residents of Pueblo Bonito. Contrary to expectations based upon population genetics theory

(Konigsberg, 1987), females exhibit greater within-group variability for both the Judd (6 of 11 variables) and Pepper (8 of 11 variables) samples. The multivariate analysis supports these findings, however, statistically significant p-values were rare. This is expected since the Type II error rate was approximately 50% for the multivariate tests. The biodistance analysis also supports these results with males exhibiting smaller average within-group inter-individual Mahalanobis distances than females.

Despite the lack of significant differences observed between males and females, the overall pattern of both phenotypic variability and biological similarity suggests a residence pattern centered on male relationships.

**Functional interpretation of the Laetoli footprints.** P. SCHMID, Anthropological Institute and Museum, University of Zurich-Irchel, Switzerland.

Examination of the Laetoli hominid footprints has already led to a diversity of opinion on different topics. Recent reconstruction of the locomotor apparatus of australopithecines led to the hypothesis that their locomotor repertoire included a significant proportion of arboreal activity. While the structure of the foot of the earliest hominids may be partially gleaned from the study of its preserved skeletal parts from sites in Eastern and Southern Africa, such fossils lack information about the weight transfer during progression.

The most important external force that acts on the body during progression is the force exerted on it by the ground. This force is due to the reaction to gravity and to the momentary acceleration of the body. The relative distribution of pressure between the lateral and the medial portions of the foot is a crucial matter, not only for the functioning of the foot, but also for interpreting the fossil footprints fixed in the ash layers at Laetoli. In bipedal movement the fore-limb is no longer used to support against gravity or to accelerate the body. The forward swing of the arm contributes angular momentum to neutralise partially that of the advancing leg of the opposite side. The arms do not behave as pendulums in typical walking but are subject to muscle action. The swinging of the arms is consequently not a purely incidental accompaniment of forward movement, but is an integral part of the dynamics of progression.

Consequently, we analysed the weight transfer of an individual in walking normally and also in walking with different constraints on arms and trunk motion during bipedal locomotion. The differences in the course of the gravitational force in the footprint can give some insight for the peculiar footprint morphology in the Laetoli trails.

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The relationships of microwear scratches and pits to occlusal macrowear. C.W. SCHMIDT and S.P. NAWROCKI, Archeology and Forensics Laboratory, University of Indianapolis, Indianapolis, IN 46227.

The relationship between dental microwear features and gross occlusal macrowear is important for characterizing paleodiets. Teaford and colleagues have suggested that hard food consumption leads to a higher percentage of microscopic pits. Our question is: do "hard" diets (as indicated by pit-laden teeth) wear away dental hard tissues more quickly than softer diets (i.e., those that produce comparatively more scratches)?

Casts of 95 human mandibular second molar Phase II wear facets were viewed with a scanning electron microscope and micrographed at a magnification of 500X. The teeth come from four prehistoric populations from Indiana, each of which represents a different temporal period: Late Archaic (n = 21), Early/ Middle Woodland (n = 21), Late Woodland (n = 30), and Mississippian (n = 23). Feature diameters and frequencies were determined using *Microware 2.2* software (Ungar, 1995). Macrowear scores were also assigned for the same molars using the Scott (1979) scoring system.

General factorial, Model I ANOVAs determined that age and sex do not contribute to differences in microwear feature expression. Spearman correlation coefficients were calculated for each microwear variable (scratch length, scratch width, pit length, and percentage of pits) vs. macrowear score. Statistically significant positive correlations between the scratch size variables and macrowear score suggest that scratch size and rate of macrowear are associated. No such relationship was found for the pit-related variables. We conclude that heavy pitting does not lead to higher rates of macrowear and that microwear patterns that are dominated by large scratches should be considered "abrasive", a distinct microwear-based dietary classification that can accompany, and contrast with, a "hard" diet.

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Variation in the timing and display of the human smile. K.L. SCHMIDT, Department of Anthropology, Indiana University of Pennsylvania, Indiana PA 15705

Human smiling, like other forms of human expression and emotion, is typically embedded within the context of social communication and display. Yet as many as two thirds of facial expressions in natural interaction occur during speech and do not directly convey the emotions of the speaker. The smile, in particular, occurs very frequently in the course of social interaction. This paper uses ethological data to address questions about how, when, and ultimately why humans smile. Detailed and objective methods of

measurement are combined with an ecologically relevant approach to human smiling behavior.

A corpus of 192 smiles obtained from dyadic interviews with 36 individuals is examined. Smiling is defined as the presence of Action Unit 12 (Facial Action Coding System) which represents the facial movement associated with contraction of the *zygomaticus major* muscle. All smiles were initially observed and coded according to their relationship with the subject's speech. Onset, apex and offset times, as well as total duration for instances of AU 12 were recorded from videotaped interviews.

Three reliably coded categories of smiles are distinguished: smiles immediately preceding subject speech (PRE), smiles discontinuous with subject speech (SM) and smiles immediately following subject speech (POST). Timing of onset, apex and offset and total smile length are compared for two of these types, SM and POST. There is substantial variation within the categories of SM and POST smiles, although the two types differ on average in frequency and duration. Differences in timing between SM and POST smile types are discussed as evidence of differing roles for these smiles in social display. Because of their frequency in social interaction and coordination with vocal activity, facial displays are important for understanding communication in humans, as well as in non-human primates.

Bayesian prediction of adult age at death assessment on multiple indicators. A.SCHMITT and C.BROQUA, Department of Anthropology, University of Bordeaux 1, Avenue des Facultés, 33 405 Talence, France

Lucy et al (1996) propose a non-parametric method based on application of the Bayes theorem to assess age at death from a dental technique. This Bayesian predictive model provides "posterior probabilities" that an individual falls in a certain age category. From these probabilities, they calculate a median age by linear interpolation. They obtain a better prediction and a smaller 95% confidence interval than by using regression techniques.

From our point of view, age prediction methodology must obtain the highest confidence on the age estimation with a moderate inaccuracy. For this reason, we use the Bayesian predictive approach on a combination of age indicators: sternal end of the clavicle, iliac crest, pubic symphysis, and auricular surface of the ilium. To apply the Bayesian approach, it is necessary to elaborate an ordinal scale for each morphological modification of the pubic symphysis and auricular iliac surface from the initial study of Suchey and Brooks (1986) and Lovejoy et al (1985).

A data set was collected from White Americans in the Hamann-Todd Collection (n=99). Every age category was equally represented. Statistical tests demonstrate no significant difference in the distribution of morphological features between sexes.

We calculate the "posterior probabilities" of each individual for belonging to a deccennial age category by using the jackknife resampling strategy. When the chosen threshold of posterior probability is 0.75 on 2 adjacent age categories at the maximum, the successful rate of age assessment of 80%. A second data set from Black Americans (n=51) in the same collection was tested, using the White sample as the predictive population, with similar results. The Bayesian predictive approach permits estimation of age at death with greater confidence without losing accuracy.

Reconstruction of stature from long bones in Native American populations. T. M. SCHÖBER, Department of Anthropology, University of Florida, Gainesville, 32611.

The variation in body proportions of Native Americans is generalized when we use a single set of linear regression formulae from a geographically and genetically distinct reference population for stature calculation. It is widely assumed that either the most statistically robust regression equations (e.g., Trotter and Gleser 1952, 1977, American Whites) or those based on indigenous North American samples (e.g., Genovés 1967) will provide the least biased results for Native American skeletal material. Unfortunately, it will never be possible to develop regression equations for specific Native American populations because the large cadaver samples necessary simply do not exist. This study proposes a statistical way of evaluating existing reference populations that will both increase our understanding of the diversity of body proportions between Native American groups and provide an objective means of choosing from stature regression equations available in the literature.

This study evaluates heterogeneity of Native American body proportions using maximum long bone lengths from five large, geographically discrete archaeological samples. I collected maximum lengths of the femur, tibia, humerus, and radius for each complete adult skeleton from the following sites/components: 1) Schild, Mississippian (n=97), 2) Pete Klunk, Middle Woodland (n=49), 3) Arikara, proto-historic (n=128), 4) Nunavut Inuit, historic (n=100), and 5) Ancon, Peru, Late Intermediate (n=76). These data are compared multivariately to all available reference populations based on American White, American Black, French, Indian, Mexican, and North and South Chinese samples. The multivariate case for each reference population is reconstituted from published means, standard deviations, and correlation coefficients. Male and female variance-covariance matrices for each reference population are pooled with similar matrices for each Native American sample. Principle components analysis is used to delineate the multivariate position of each Native American sample in relation to all reference populations.

I argue the reference population(s) that is most similar to Native American material for all major long bone lengths, regardless of genetic or geographic similarity, is the most statistically valid model for stature estimation. This study demonstrates that the diversity in Native American body proportions are not represented by a single reference population. Patterned differences in limb segment length relationships exist, and must be taken into account prior to stature estimation.

The effects of different brain indices on brain/behavior relationships: a within-species study of humans. P. THOMAS SCHOENEMANN, Department of Anthropology, University of Pennsylvania, Philadelphia, PA 19104-6398

It is well known that brain size scales with body size. Various indices have been proposed that allow for the estimation of brain size independent of body size (e.g., Jerison's "encephalization quotient" or EQ). An implicit assumption is sometimes made that these body size corrected brain measures are a better measure of inherent behavioral differences than are simple differences in absolute brain size. This may partly be due to the fact that, for both absolute brain size and brain-size-as-a-percentage-of-total-body-weight, *Homo sapiens* do not exceed other species, even though we are clearly extremely successful mammals on purely behavioral grounds. Some research, however, is consistent with the idea that absolute brain size, in and of itself, has important behavioral implications. In addition, some comparative brain/behavior studies have used indices which scale one part of the brain with the some other part (or the brain as a whole). In any case, which brain indices are the most important behaviorally is an empirical question that can only be decided with actual behavioral data: a given brain index might be more highly associated with some behavioral dimensions than it is with others, and some brain indices might be more highly related to particular behavioral dimensions than are other indices.

This raises the question of whether brain/behavior correlations in humans might differ significantly depending on how brain variables are scaled. The present study addresses this issue by assessing whether different brain indices vary with respect to their associations with different behavioral measures. Brain size (obtained from high resolution MRI) and behavioral variability (assessed through a battery of cognitive and behavioral tasks) were obtained from 72 healthy human females. Correlations were then calculated using different brain indices. The results suggest that the use of different scaling measures does not significantly affect the strength of brain/behavior associations within humans. The implications of these findings for understanding hominid brain evolution will be discussed.

A comparison of osteoarthritis in the appendicular joints of males from the Hamann-Todd and Terry Collections. J.J. SCHULTZ, C.A. Pound Human Identification Laboratory, Department of Anthropology, University of Florida, Gainesville, FL 32611.

The Hamann-Todd (HTC) and Terry Collections (TC) are used extensively as control or reference groups in many studies of biological variation and pathological analysis. In fact, they have served as essential databases for developing many of the analytical techniques used currently by skeletal

biologists. However, only a few references directly compared the two samples, and there have never been any studies making direct comparisons of pathological lesions between the two collections. Although there have been studies by different workers focusing on osteoarthritis in both collections, the results are not comparable due to different scoring methods. Therefore, the purpose of this study is to test whether these collections represent a homogeneous population with respect to appendicular osteoarthritis.

The skeletal sample in this study includes 290 white and black males from both collections: 146 from the HTC and 144 from the TC. Individuals were chosen equally from four 15-year groupings (25-39, 40-54, 55-69, and 70+). Marginal lippling was scored on the elements of the right and left shoulder, elbow, hip, and knee. The scoring method employed in this study combines the degree and the extent of the lippling into one category represented by one numerical score ranging from 1 to 9. ANCOVA was then performed to compare the lippling scores between the independent variables age, ancestry, and museum. To supplement this analysis raw scores were grouped into descriptive categories (absent/slight, moderate, and severe) in order to compare the frequency of osteoarthritis.

Results show that differences between the two collections are significant at the elbow and knee, being most severe in HTC males. Other joints fail to display significant differences by collection. Ancestry is not a significant factor in the expression of marginal lippling at any joint. Finally, the most important variable affecting the expression of marginal lippling in both collections is age at death.

Infectious diseases of subadult age in prehistoric and early historic Europe and the Near East: etiology and epidemiology of diseases. M. SCHULTZ, P. CARLITHE, AND T.H. SCHMIDT-SHULTZ, University of Göttingen, Göttingen, Germany.

The occurrence and the intensity of diseases are strongly influenced by living conditions. Within ancient populations, children and particularly infants, as well as senile individuals were the weakest groups of a community, especially with respect to diseases and other environmental factors. Thus, nature and frequency of diseases in the subadult age are a relatively reliable indicator of the skull which produce characteristic vestiges, present a wide variety in morphology. However, using different techniques such as microscopy, diagnoses are made relatively reliably.

It is striking that some diseases are apparently characteristic of poor living conditions, such as inflammatory processes of the paranasal sinuses, otitis media and mastoiditis. For instance, the incidence of these diseases is three or four times higher in the social lower classes. Populations that had a high frequency of deficiency diseases, also frequently suffered from inflammatory diseases: in the state of malnutrition, the immune response is insufficient. In osteomyelitis of the external skull vault, inflammatory processes of the postcranial skeleton are relatively frequently seen. This could be explained by a generalized sepsis due to poor living conditions. Differences in ecology probably induce different patterns of diseases (e.g., meningitis).

The Robusticity-Gracility Debate: Temporal Trends in European Cranial Morphology. B.A. SCHUMANN, Department of Anthropology, Florida Atlantic University, Boca Raton, Florida 33431

For years, claims have been made concerning and supporting the notion that there are changes in cranial morphology throughout the European Upper Paleolithic. These changes have been characterized by gracilization, whereby there is a clear reduction in the degree of robusticity from early to late Upper Paleolithic specimens. Analyses of both metric ( $n=21$ ) and nonmetric ( $n=9$ ) variables, 45 fossils and 317 modern Europeans (Howells' populations) demonstrate that gracilization is not a characteristic of cranial change during the European Late Pleistocene.

A one way analysis of variance of metric variables demonstrated that 38% ( $n=8$ ) of these variables were significantly different at the  $p=0.05$  level when comparing early and late specimens. Four of these variables are measures of cranial and facial breadth while the remaining four are measures of cranial length, indicating that there are overall differences in cranial size throughout this period. This result is supported by a multivariate factor analysis which separates early from late specimens based on measures of breadth and length, further support for the conclusion that changes in cranial morphology throughout this period are ones of size and not robusticity. Furthermore, it is differences in size which separate the Upper Paleolithic specimens from recent Europeans.

The evaluation of nonmetric traits scored as grades, such as supraorbital torus development and the degree of lambdoid protrusion, can indicate directly changes in the level of cranial robusticity. As only one out of nine of such variables changes throughout this period, it is clear that gracilization, or the reduction in robusticity, is not a characteristic of this period.

While there are significant changes throughout the Upper Paleolithic in cranial morphology and significant differences between this period and modern Europeans, these changes cannot be characterized by a reduction in cranial robusticity but merely changes in overall cranial size.

Mitochondrial DNA diversity in lower Amur River populations, and its implications for the genetic history of the North Pacific and the New World. T.G. SCHURR<sup>1</sup>, E.B. STARIKOVSKAYA<sup>2</sup>, R.I. SUKERNIK<sup>2</sup>, A. TORRONI<sup>3</sup>, D.C. WALLACE<sup>4</sup>. <sup>1</sup>Southwest Foundation for Biomedical Research, San Antonio, TX. 78245-0549; <sup>2</sup>Institute of Cytology and Genetics, Novosibirsk 630090, Russia; <sup>3</sup>Dipartimento di Genetica e Biologia Molecolare, Università di Roma "La Sapienza", Rome, Italy, 00185; <sup>4</sup>Center for Molecular Medicine, Emory University School of Medicine, Atlanta, GA. 30322.

Due to its abundant resources, and because of its relative proximity to the crossroads of northern Asia and the New World, the lower Amur River region has been suggested as the potential homeland for the first wave of ancestral Amerindians, as well as plausible route through which immigrant populations from the Siberian/Asian interior may



have expanded into contiguous Beringia and then northern North America. However, to date, very few studies of mtDNA variation in lower Amur River peoples have been conducted. Our own work in this part of Siberia has shown the Udegeys of the Sikhote-Alin Range and the Nivkhs of northern Sakhalin Island to have unique genetic profiles, while also having affinities with either Tungusic or Paleoasiatic populations, respectively. Yet, these two populations represent only a portion of the ethnic diversity present in the lower Amur River region. To further elucidate the population histories of the culturally and linguistically diverse hunting/fishing groups which have inhabited this region since the Neolithic, we performed RFLP and control region (CR) sequence analyses of mtDNAs from the Ulchi, Nanai, and Negidals of the Lower Amur Basin. In addition, the Nivkh and Udegey mtDNAs that had previously been subjected to RFLP analysis were surveyed for CR sequence variation. The resulting data were then compared with similar Siberian and Native American data sets. Our results suggest that the lower Amur River region may have played a role in the dispersal of ancestral Native American populations, and that its inhabitants have been genetically influenced by populations from both eastern Siberia and East/Southeast Asia.

Heavy metal burden in ancient miners and metal workers – biomonitoring through archaeometry. H. SCHUTKOWSKI, Historical Anthropology and Human Ecology, University of Göttingen, Germany.

As a result of technological development and progressive urbanization, environmental pollution caused by the emission of anthropogenic harmful substances was increasing in continental Europe since High Mediaeval times. In particular, mining and the processing of metals led to an influx of these substances into the biosphere. Even today, this is detectable in terms of geochemical hot spots, environmental alterations, which by far exceed the amount of naturally prevailing element concentrations. The impact on conditions of living and health can be reconstructed in past populations by the determination of heavy metal concentrations in archaeological bone. Such an archaeometrical approach allows to recognize and evaluate possible accumulations of harmful substances and may thus contribute to a historical biomonitoring.

Skeletal samples from traditional German mining areas, here: 18<sup>th</sup> century *silvani* (i.e. ore smelting workers) from the city of Goslar in the Harz mountains, and 13<sup>th</sup> century *montani* (i.e. mining workers) from Sulzburg in the Black Forest, were subjected to trace element analyses of lead, cadmium, arsenic and antimony. The samples are part of populations known to have made their living from mining and ore smelting. Therefore, they represent those rare cases, in which an empirically detected heavy metal burden can be directly correlated to occupational activities. Element concentrations show values which characteristically increase with age, thus reflecting a continuous exposition during lifetime. Lead concentrations were found to be many times over known adaptive pre-industrial values. A conspicuous lack of gender differences points to similar

patterns of exposition to hazardous substances. The results will be discussed with reference to both their historical significance as well as their possible implications for public health.

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**The Ontogeny of Canine Dimorphism in Extant Hominoids.** GARY T. SCHWARTZ, The George Washington University & Human Origins Program, NMNH, Smithsonian Institution, Washington, D.C.; CHRISTOPHER DEAN, Evolutionary Anatomy Unit, University College London, London, U.K.

Despite much information, comparatively little evidence points to differences in any aspect of dental development among the three genera of great apes. For canines, for example, most studies suggest that males and females initiate mineralization around the same time (around birth) continuing until nearly 11 years of age in all great apes. If crown formation times (CFT) are the same in males and females, is greater canine height in males due to differences in *rates* of growth? Or are rates of growth similar between sexes within each species, so that differences in the *period* of growth account for the observed dimorphism in canine height? To pinpoint the precise developmental mechanisms underlying canine dimorphism, we undertook a histological study of a total of 115 great ape (*Pan troglodytes*, *Gorilla gorilla*, and *Pongo pygmaeus*) and human mandibular canines of known sex. Thin sections (100-120µm) were prepared from the midline axial plane exposing the entire buccal aspect of each crown, thereby encompassing the entire period of crown formation. Sections were examined using polarized light microscopy and photomontages (x250) to record intra- and interspecific variations in periodicity, daily secretion rates, enamel thickness and total CFTs.

Interspecific comparisons reveal that *Gorilla* and *Pongo* canines achieve taller crown heights than *Pan* through *rate* hypermorphosis over the whole growth period. The initial rates of growth in tooth height are faster in human canines than in *Pan* but crown formation completes more quickly in humans. Intraspecific tests show that male ape canines grow for longer than females for all species; males can take up to 10 years in *Gorilla* and *Pongo*, nearly twice that of some females. Slight differences in the overall *rate* of canine growth also contribute to differences between the sexes in each species. Unlike great apes, human canines show no clear evidence of *time* hypermorphosis to account for small amounts of sexual dimorphism in crown height.

Growth curves for male ape canines differ from those of females in that they follow a tighter trajectory, which is consistent with males being under greater selection pressure. This model offers some prospect for a developmental correlate that reflects social organization in primates and provides the first comparative developmental framework for interpreting canine size/dimorphism in early hominids.

**Discriminant function analysis of skeletal teaching collections: population specific sex differences?** A.L. SCOTT, New Mexico State University.

For many years, biological supply companies purchased human remains from Indian or

Pakistani processing companies for resale to Western schools, universities, and educational institutions. Existing formulae cited in textbooks and lab manuals are based primarily on American blacks and whites. Many of the skeletons provided to biological supply companies are gracile as a result of regional human variation, inadequate nutrition, or lower socioeconomic status. Because of this gracile nature, the formulae based on American skeletons do not provide accurate results. The purpose of this study is to question the applicability of these formulae to skeletons of Indian or Pakistani origin, on which many students of physical anthropology learn to determine sex. Furthermore, this study will suggest whether new formulae need to be adopted in the classroom.

The sample for this study consists of over 100 individuals purchased from biological supply companies and used in U.S. universities for teaching purposes. The researcher established the sex of each individual using visual techniques for the pelvis. Measurements were taken from the humeri, radii, ulna, femora, and tibiae of each individual, and from these measurements new discriminant formulae were produced. These new formulae are compared to the existing ones and their potential application is examined.

Comparative paleoecology of *Dryopithecus* and *Ankarapithecus*. R.S. SCOTT<sup>1</sup>, R. BERNOR<sup>2</sup>, and T. KAISER<sup>3</sup>. <sup>1</sup>Dept. Anthropology, University of Texas, Austin, TX 78712-1086, <sup>2</sup>Dept. Anatomy, Howard University, Washington D.C. 20059, <sup>3</sup>Institute and Museum of Zoology, University of Greifswald, D-17489 Greifswald, Germany

The Late Miocene is marked by the immigration of hipparionine horses into the Old World at the beginning of MN9 (ca. 11.2 Ma) and their apparent rapid geographic expansion and evolutionary radiation. This radiation co-occurs with MN9 Eurasian hominoids which mostly go extinct by MN10 times. Thus, for a brief window in the late Miocene, a hipparionine radiation coexisted with biogeographically diverse hominoid genera. That this period of time may represent a window of unique or changing ecological circumstances is supported by evidence of two late Miocene global cooling events. One is dated to between 10.9 Ma and 9.8 Ma while a second more severe event corresponds to between 9.4 and 8.37 Ma. Thus, the first event is correlative with hipparionine radiation and possibly earlier hominoid extinctions, while the second event is correlative with the last hominoid extinctions.

Recent hominoid finds of *Dryopithecus* at Rudabanya in Hungary and *Ankarapithecus* at Sinap in Turkey will increase our understanding of this critical period of hominoid evolution and further emphasize the importance of understanding the paleoecology of this time period. We have investigated hipparion metapodials from these two sites from an ecomorphological perspective as a means of

reconstructing the types of habitats that may have been available to these hominoids regionally. Both sites include elongate metapodials suggesting possible cursorial adaptations. The smaller sample size available from Rudabanya increases the uncertainty associated with the analysis. However, it does suggest the intriguing possibility that the Rudabanya fauna may include hipparion species with cursorial adaptations that may have used a range of habitats including ones distal to the late Miocene Pannonian Lake. In general, these results contribute to a view of general 'patchiness' of habitats at various geographic scales during the Vallesian. Habitats available to the Vallesian Eurasian hominoids may have indeed been diverse, complex, and in flux.

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#### African Ape Nuclear Phylogeography

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Several previous studies have taken a phylogenetic approach to the study of biogeography in African apes and humans using mitochondrial DNA. Here we report on the first study to examine genetic diversity in the nuclear autosomal genome in all currently recognized species and subspecies of living African (or African-derived) hominoids: (*Homo sapiens*, *Pan troglodytes troglodytes*, *P.t.schweinfurthii*, *P.t.verus*, *P.paniscus*, *Gorilla gorilla gorilla*, *G.g.graueri*, and *G.g.beringei*). We compare and contrast these results with those from the mitochondrial genome, and place the results in a biogeographical perspective.

Three noncoding loci (near the genes ADH, DRD4, and HOXB6) were examined for all nucleotide sequence variation in a region of approximately 600bp (ADH) and 1,000bp (DRD4 and HOXB6) in representatives from all African ape subspecies. These loci were chosen without prior knowledge of the amount of variation in any taxon, and therefore free from ascertainment bias. For most taxa at most loci, at least 5 individuals (10 chromosomes) were sampled, although fewer than 5 *P.t.schweinfurthii* and *G.g.beringei* were sampled. For individuals heterozygous at multiple positions at a locus, molecular haplotyping methods were used to resolve their phase.

In general, humans show less genetic diversity than chimpanzees or gorillas—consistent with previous mtDNA studies—but in contrast with some previous studies based on nuclear microsatellites. The most obvious contrast between the mitochondrial and nuclear results are in the relationship between western lowland gorillas (*G.g.gorilla*) and the two eastern subspecies (*G.g.graueri* and *G.g.beringei*), with mtDNA showing a very ancient split and nuclear DNA suggesting much more recent gene flow between these subspecies.

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A comparative craniofacial analysis of 24 Asian and Pacific populations using the neighbor-joining method. N. SEGUCHI and C.L. BRACE, Museum of Anthropology, University of Michigan, Ann Arbor, MI. 48109.

Recent and prehistoric human craniofacial samples in 24 Asian and Pacific populations representing a broad geographic area were compared using the neighbor-joining method (Saitou and Nei, 1987). The neighbor-joining tree was constructed on the basis of Euclidean distance matrix computed by weighted mid-sex C scores from 21 craniofacial-metric variables. In addition, the degree of support of the branches was tested by a bootstrap analysis (bootstrap size=1000).

The three major divisions of the tree are observed amongst: 1) prehistoric Jomon, Hokkaido Ainu, Polynesian, medieval Kamakura, and modern Ryukyu people; 2) Yayoi, Mongol, Chukchi, Northern Chinese, Manchu, Chinese Neolithic, Korea, Northeast Chinese, Modern Japanese, China Bronze age, and China Nanning; and 3) Thai modern, Burma, Philippine Manobos, Dayak, Taiwan, Sumatra Batak, Atayal, and Sepik River Papua New Guinea. However, Atayal and Papua New Guinea show another separation within the third group.

Within Japan, two distinct morphological groups are observed. One is the cluster of the Jomon, modern Hokkaido Ainu, medieval Kamakura, and modern Ryukyu. Another is the Yayoi and the modern Japanese which belong in the East and northeast Asian group.

In the first group, the Jomon and Hokkaido Ainu cluster show a high bootstrap value (100 %), and the Jomon and Hokkaido Ainu cluster and Polynesian show a medium bootstrap value of 43.4 %. In the second group, the Manchu-Chinese Neolithic cluster shows a high bootstrap values (75 %), and the Mongol-Chukchi cluster, and the Korea-Northeast Chinese cluster show moderate bootstrap values (65.2 % and 56.6 %).

Although the low bootstrap values indicate a lack of structure in the tree, the Jomon-Hokkaido Ainu-Polynesian cluster is related to the Northeastern Asian populations. It similarly shares the cluster of the Austronesian Language speaking families such as Batak, Atayal, and Dayak.

Exo- and endocranial morphometrics and the implications for mid-Pleistocene crania descriptions. H. SEIDLER, K. SCHAEFER, H. PROSSINGER, G.W. WEBER  
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We present a study of a morphometric analysis of modern humans and fossil crania (*H. heidelbergensis*: Bodo, Kabwe, Petralona & Atapuerca 5 and *H. neanderthalensis*: Guattari) by defining a suite of exo- and endocranial landmarks, whose 3D positions were measured. The 3D positions of the fossil data were measured on stereolithographic models of these crania. Using the new morphometrics (Procrustes shape and principle warp analysis), we find significant and unexpected differences. Using the Procrustes size as a scaling variable, we compare various linear dimensions between recent and fossil crania,

particularly those that reflect the size of the frontal sinuses and the thickness from inion to endo-inion, the latter suggesting interesting implications about the position of the cerebellum. Our analysis shows that, of the fossil specimens, Atapuerca 5 is unusual when compared to the others from the *H. heidelbergensis* group. The (unscaled) distance from foramen caecum to endo-inion in the fossil specimens lies well within the range of modern humans. We also present shape variable statistics that show significant differences and remarkable similarities between the recent and fossil specimens: particularly striking are some shape affinities between Atapuerca 5 and Guattari.

Variation in age at weaning in pre-industrial societies. D.W. SELLEN, D. B. SMAY and L. LIBARIDIAN,  
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Cross-population studies reveal broad quantitative associations between subsistence practice and demographic parameters for pre-industrial populations. It is plausible that the observed variation in infant mortality, birth spacing and fertility rates may have been associated with variation in weaning practices, but few studies have developed and tested predictions about the cross-cultural relationship between key measures of subsistence activity and key indicators of the weaning process. We suggest patterns of weaning may have differed systematically across populations engaged in different types of subsistence because of differences in availability of weaning foods, differences in maternal time allocation to subsistence work versus care of young children and/or differences in the optimal solution to the weanling's dilemma. Using reports from the literature, we conducted a cross-cultural test of the "weaning food availability hypothesis": that weaning was initiated earlier in agricultural and pastoral populations because dairy and cereal production increased the availability of easily digestible, nutrient-rich foods appropriate for weaning. Contrary to predictions, the results indicate significantly delayed supplementation with non-breast milk liquids in more agricultural, and marginally delayed complementation with solid foods in more pastoral, populations. Duration of breastfeeding increased among populations more dependent on hunting, but not fishing or gathering. Such patterns are more consistent with the alternate "maternal work pattern" and "shifting weaning optimum" hypotheses. Markers of weaning show some association with maternal work organization and with pathogen risk. We discuss the implications for understanding the mechanisms underlying pre-historic human demography, subsistence shifts, allocation to parenting versus mating effort and the evolutionary implications of trade-offs between diet and disease.

The effect of group size on proximity and patterns of affiliation in the Milne-Edward's sifaka (*Propithecus diadema edwardsi*) in Ranomafana National Park, Madagascar. R.G. SELTZER, Department of Anthropology, Kent State University, Kent, OH 44240 and P.C. WRIGHT, Department of Anthropology, SUNY at Stony Brook, NY 11794

Proximity has been used to measure patterns of affiliation as well as the presence and intensity of feeding competition among nonhuman primates. In the Milne-Edward's sifaka, no differences in proximity were found among three group members when sex, age, and kinship were taken into consideration (Seltzer, 1999). This finding may have been influenced by the possible lack of intense feeding competition in a small group size during periods of food abundance. During seasons of food scarcity, however, Overdorff et al. (1999) found that diet and bout length differed with regard to age, sex, and reproductive status in this species. This suggests that these sifakas may respond to feeding competition when resources are scarce. The focus of this study was to examine the effect of group size on proximity in the season of abundant fruit and the season of scarce fruit and to analyze any patterns of proximity that were associated with the age, sex, or kinship of the group members.

Three groups of Milne-Edward's sifakas were observed over a seven year period in Ranomafana National Park, Madagascar. Group size varied within groups from three to nine individuals. Samples were taken in five minute intervals to record the distance and the identity of group members within five meters of the focal animal during feeding, resting, and traveling. We found that indeed proximity decreased with fruit scarcity. In addition, proximity decreased with an increase in group size, regardless of season. Data on nearest neighbor identity were then analyzed for sex, age, and kinship patterns. Females were closer to other group members than males when group size was greater than three. Female infants and juveniles had greater proximity than male infants and juveniles. No significant patterns of kinship emerged. These results support the prediction that groups become more dispersed as group size increases, especially in the season of scarce resources.

The evolution of the frontal cortices in the Plio-Pleistocene: new evidence. K. SEMENDEFERI<sup>1</sup>, A. LU<sup>1</sup>, A.M. DESGOUTTES<sup>1</sup> and H. DAMASIO<sup>2</sup>, Dept of Anthropology<sup>1</sup>, UCSD, La Jolla, CA 92093 and Dept of Neurology<sup>2</sup>, University of Iowa, IA 52242.

A popular idea that dominated the literature of the 20<sup>th</sup> century has been that the frontal lobes and the frontal cortices of the human brain enlarged disproportionately during human evolution. Cognitive capacities like abstract thinking and language, known to involve the frontal lobes, have been mostly attributed to this disproportionate enlargement. The notion of this uniquely large human frontal lobe was based on scarce primary data collected

earlier in the century with limited quantitative tools and has not yet been tested convincingly.

We started by investigating the size of the hominoid frontal lobe as a whole (Semendeferi et al., 1997; Semendeferi & Damasio, 1999) and documented that the human frontal lobes are not larger than expected for an ape brain of human size. Humans and great apes (but not other primates) have overlapping relative values (33-39% of the volume of the hemispheres).

Here we explore the possibility that it may not be a disproportionate increase in the size of the frontal lobes that distinguishes the human brain from the great and lesser apes, but rather a disproportionate increase in the cortex of the frontal lobes. We also investigate the size of three sectors of the frontal cortex, the dorsal, mesial and orbital sectors, in great and lesser apes and we address the question of the evolution of the frontal cortices in the hominid line. MR scans of 29 living subjects are included (10 human, 19 great and lesser apes).

Contrary to traditional wisdom, human frontal cortices are not larger than predicted for an ape brain of human size. The values for the relative size of the frontal cortex as a percentage of total cortex are similar in humans and great apes. The range of relative values of individual subjects overlaps in humans and great apes, but is smaller in lesser apes. The relative size of the orbital sector is considerably smaller in the orangutans than in any other hominoid.

Disproportionately large frontal lobes and frontal cortices are not a hallmark of hominid brain evolution, but are shared features that may have appeared during the Miocene. Smaller sectors of the frontal lobes have become specialized during ape and human evolution.

Craniofacial dimensions in small anthropoids and prosimians. K. SHAHMOHAMMADI and J. RUNESTAD CONNOUR, Department of Biological Sciences, Western Illinois University, Macomb, IL

This study explores the effects of phylogeny and function on craniofacial anatomy in small primates. Several skull dimensions were measured for members of Callitrichidae, Tarsiidae, Galagonidae, Loridae, and Cheirogaleidae.

Most of the measurements were taken with digital calipers. Cluster analyses were performed to identify natural groupings in the data. The effect of body size on cluster formation was explored by plotting variable values against body mass in bivariate plots. Further analysis with quantitative techniques is planned.

The most interesting results are for callitrichids and tarsiids. They share short basicranial length and wide postorbital width. Callitrichids are unique in having more rectangular palates, smaller eye orbits, and more cranial roundness between the bregma and opisthion than the other primates. Tarsiids are unique in having more triangular palates, closer together eye



orbits, and larger eye orbits than the other primates.

Cheirogaleids, galagonids, and lorids overlap for most of the variables, with a few exceptions.

While many of these characteristics probably reflect ancestral relationships, some can also be explained functionally. For example, Callitrichidae have relative small eye orbits, as is expected from their diurnality. The large, close eye orbits of tarsiers correspond to their nocturnality and lack of a tapetum lucidum. Also, the triangular palates of tarsiers may be linked to their completely faunivorous diet. It is proposed that this shape provides a biomechanical advantage for biting.

The role of lateral bending of the spine in prosimian quadrupedalism. L.J. SHAPIRO, University of Texas, Austin, TX 78712, B. DEMES, SUNY at Stony Brook, NY 11794, and J. COOPER, Purdue University, W. Lafayette, IN 47907

Much research has been devoted to spinal kinematics among non-mammalian vertebrates, while comparatively little is known about the role of spinal movements in mammals, especially primates. This study, conducted at the Duke University Primate Center, examines the function of lateral spinal bending in quadrupedal walking among a diverse sample of prosimians. The sample includes *Loris tardigradus* (1), *Nycticebus coucang* (1), *Nycticebus pygmaeus* (1), *Cheirogaleus medius* (2), *Varecia variegata* (2), *Eulemur fulvus* (2), and a total of 238 strides.

Lateral flexion at touchdown is more pronounced in both species of *Nycticebus* than in all of the other taxa, and *Loris* and *Cheirogaleus* use more flexion than do the lemurs. Some of these differences may be influenced by variation in the timing of flexion relative to touchdown across taxa. The heterogeneity within the lorids is notable in light of their distinctions in vertebral morphology.

Velocity effects are significant only for the smaller taxa, within which there is an interesting contrast between lorids (particularly *Nycticebus pygmaeus*) and cheirogaleids. At higher velocities, lateral flexion becomes less pronounced in cheirogaleids but more pronounced in lorids. This result is intriguing, because the cheirogaleid pattern is presumably characteristic of lizards and mammals, whereas the lorid pattern is more amphibian-like.

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Allometry and Size Control in Primate Morphometrics B.T. SHEA, Northwestern University, Chicago, IL 60611.

Many researchers agree that morphometric analyses should in principle attempt to assess and control for the influence of variation in body size within the comparative sample at hand. Yet the most appropriate methods of controlling for these allometric influences are continually debated, leading some to suggest alternative methods rooted in geometric scaling. These central issues in comparative morphometrics are investigated here using datasets of postcranial and cranial proportions in ontogenetic and interspecific analyses of african cercopithecoids and hominoids. The goal is to investigate how alternative approaches to size correction account for allometric and non-allometric influences on interspecific morphological variation. Allometric influences here comprise both ontogenetic scaling and biomechanical scaling, with the latter hypothetically contrived to account respectively for none, some and all of the interspecific shape differences residual to the allometric factor of ontogenetic scaling. Alternatively, residual shape variance in interspecific adult analyses is determined following correction against an isometric size axis. Comparative results of these two approaches indicate that size assessment relative to an axis of isometric change in fact fails to effectively detect allometric influences. Moreover, this approach conflates the dual and distinctive causal allometric inputs of (1) different endpoints along shared trajectories of relative growth (ontogenetic scaling); and (2) repatterning of ontogenetic trajectories to maintain some meaningful criterion of functional equivalence at varying sizes (biomechanical scaling). These results also demonstrate that simple interspecific regression fits taken as generalized criteria of subtraction in fact conflate true causal allometric influences with non-allometric influences spuriously correlated with overall size. I advocate a more biologically-meaningful "criterion of residualization", this one phylogenetically-based and allowing for the detection of derived restructuring of ancestral patterns of covariance (allometric or otherwise). The assessment of allometric influences in morphometrics resembles that of detection of phylogenetic influences, being scientific hypotheses that over time become more or less corroborated.

**The sagittal suture and bilateral symmetry: implications for australopithecine endocranial reconstruction.** C.C. SHERWOOD, M.S. YUAN, F.X. SUBIAUL, and R.L. HOLLOWAY, Department of Anthropology, Columbia University, New York, NY 10027 and NYCEP

The human fossil record is rife with fragmentary crania which yield incomplete endocranial reconstructions. Endocranial reconstruction depends upon the assumption of bilateral symmetry. For example, in this laboratory's

reconstruction of the SK 1585 *Paranthropus* endocast it was found that final cranial capacity estimates are highly sensitive to midline selection. Therefore, it is critical to test whether a common endocast midline landmark, namely the sagittal suture, in fact bisects the endocast into symmetrical hemispheres.

*Gorilla gorilla* (n=11), *Pan troglodytes* (n=8), and *Pan paniscus* (n=8) endocasts were selected from Holloway's collection. These taxa were chosen for their similarity to australopithecines in size and morphology. Endocasts were placed on an endocranionometer with frontal and occipital poles defining the horizontal plane. The sagittal suture was identified on each endocast and fixed as the midline for measurement. The distance from the midline to the convexity of the endocast was sampled at 10mm intervals along the horizontal plane rostral and caudal to bregma. The mean difference between homotypic points was calculated for each endocast to create a "midline error" (ME) value. Paired-samples t-tests were performed to test for symmetry.

Mean ME for the pooled sample is 0.05 and there are no significant lateral differences ( $p=0.135$ , 2-tailed). Analyzed separately, *G. gorilla* is the only species with a ME above the 0.05 level (0.07), with males showing a significant right hemisphere dominance ( $p<0.001$ ). We conclude that the sagittal suture is an unbiased midline and may be used in fossil australopithecine reconstructions. Future studies of this kind need to be conducted to test the underlying assumptions employed in endocast research.

The status of early *Homo*. R.J. SHERWOOD, Dept. of Anthropology, University of Wisconsin, Madison, WI 53706-1393, R.L. MAY, Dept. of Biology, Morning-side College, Sioux City, IA 51106-1751.

Systematists have routinely recognized the difficulty in defining higher systematic categories. Recently, Wood and Collard, (1999, *Science* 284:65-71) discussing the adaptive coherency of hominid genera, suggested that two species usually considered as members of the genus *Homo*, *H. habilis* and *H. rudolfensis*, be removed from that genus and placed into *Australopithecus*.

Their definition describes members of a genus as belonging to an adaptive zone. For hominids six criteria are presented to justify generic placement of a species within *Homo*. We would like to discuss three of these:

1) Body size. Wood and Collard present body weights as combined-sex point estimates for species without regard for the error inherent in body size estimates. Additionally, body size is used, implicitly, to describe life history strategies. The compounded error of this procedure renders the conclusions highly questionable.

2) Limb proportions. Two of the six criteria, body proportion equivalence and locomotor preference, are based largely on limb proportions. Aside from small number of specimens used to make these claims, the redundant use of a single trait biases the conclusion.

3) Developmental differences. While discussion of *Australopithecus* development includes reference to dental and femoral studies, data from the latter study indicating a similarity between early *Homo* and *H. sapiens* is ignored.

Definitions of higher taxonomic categories are always somewhat subjective. Mayr (1942) noted that, while based on natural phenomena, "the genus of the systematist is his own artificial creation, and not a natural unit." (p.290). The concept of adaptive coherency to identify congeners makes biological sense. We, however, are not convinced the criteria presented by Wood and Collard provide sufficient cause for removing *H. habilis* and *H. rudolfensis* from the genus *Homo*.

Assessing pigments in human skin and hair: New phenotypes and methodologies. M.D. SHRIVER, H. NORTON, E. PARRA, L. JIN, R.A. KITTLES. Department of Anthropology, Penn State University

As the study of the genetics of human pigmentation advances it is necessary to reexamine the methods that can be used to assess pigmentation level and ask what other phenotypes may be informative regarding the evolution and function of the skin. What exactly can be measured about the skin using reflectometry? How do different methods and instruments for spectroscopy compare and contrast? Can the two melanin types (pheomelanin and eumelanin) be distinguished in hair and skin? How much variation is there in skin response to UVA and UVB and how is skin response accurately assayed? We have addressed these questions using three different types of reflectance spectrophotometer (Photovolt ColorWalk, the Cortex DermaSpectrometer, and the Data Color International Microflash) and three different analytical methods (tristimulus colorimetry, narrow-band reflectance spectroscopy, and apparent absorbance). Using these instruments and methods we have measured the pigment levels in the hair and the skin of biogeographically diverse samples of persons living in Pittsburgh & State College, PA, Washington, D.C., and China. There are strong correlations among the results of the different methods, however there are also some important differences. Briefly, methods based on broad transmission filters (like tristimulus colorimetry and most of the previously common spectrophotometers) are confounded by increased hemoglobin levels, while narrow-band absorption methods are not. Notable is the ability of the true spectrophotometer using apparent absorption methods to distinguish among types of melanin. In addition to studying a static phenotype like pigmentation level, we are investigating skin response to UVR. Using a Solar Simulator (Solar Light Co.) subjects can be exposed to measured amounts of UVR (either UVA only or UVA + UVB). The skin response in terms of both erythema (redness) and tanning can then be determined at standard points in time. Although the general trend is for erythema to be inversely correlated and tanning correlated with basal pigment level, many persons do not fit, presumably as the result of genetic variation.

**Growth and development of enslaved Africans in Colonial New York.** K.J. SHUJAA, University of Pennsylvania, Philadelphia, PA 19104, M.E. MACK, C. J. TERRANOVA, D.C. LAMBERT, Howard University, Washington, D.C. 20059.

This study examines the patterns of growth and development among subadults and adults of the New York African Burial Ground population. Skeletal analysis reveals significant differences between dental development rates, generally considered to be the most accurate indicator of subadult age, and rates of bone ossification, growth and fusion. Infants and children frequently exhibit evidence of delayed growth and maturation, whereby ages ascertained through the evaluation of bone ossification, long bone length and epiphyseal union lag behind dental developmental ages.

Human growth and development is a complex process, involving the interaction of genetic factors and physical and cultural environments. The events associated with skeletal growth and development occur across a wide range of variability. However, historical evidence and skeletal analysis strongly suggest that observed inconsistencies between bone and dental ages among subadults are attributable to the severe environmental stresses endured by these individuals. Premature mortality and infectious disease rate were high. Furthermore, approximately 80% of the children exhibit enamel defects resulting from the disease environment.

Ongoing research continues to investigate the relationships between childhood and adolescent stress and delayed growth and maturation.

**Maternal and newborn morbidity and mortality: a report from rural northern India.** L.M. SIBLEY, American College of Nurse-Midwives. L. CALEB-VARKEY, J. UPADHYAY, S. BHARTI, Study co-mangers for Community Partnerships for Safe Motherhood, American College of Nurse-Midwives.

Nearly one quarter of the estimated 585,000 maternal deaths occurring globally each year take place in India. Increasing access to essential obstetric care will significantly reduce such loss. As part of the USAID-funded PRIME Project, Special Projects Section of the American College of Nurse-Midwives has developed "Community Partnerships for Safe Motherhood". This innovative strategy is designed to reduce maternal and neonatal mortality by increasing access to basic life-saving interventions in the home and community, reducing delays in transport to referral units where life-threatening complications can be managed, and promoting postpartum and post abortion family planning.

This strategy is being tested as a 36-month feasibility study in rural Maitha block, Kanpur Dehat district of Uttar Pradesh, India. Working with the PRIME Regional Office and Shramik Bharti, a local Indian NGO, we use a quasi-experimental design to test the hypothesis that participation in the project interventions will lead to improvements in 1) use of key preventive practices, 2) basic knowledge for survival, and 3) response to life-threatening maternal and neonatal health problems. Phase one involves gathering baseline and diagnostic information for use in community planning, development of

relevant interventions and for follow-up evaluation. This paper explores the baseline data on the Morbidity and Performance Assessment or MAP portion of this project.

MAP assesses probable medical causes, as well as social and economic factors contributing to illness and death by focusing on a woman's background and reproductive health care decision-making and the referral process in the event of a life-threatening complication. MAP includes enumeration and screening of 3753 households for eligible cases, cross-sectional survey using in-depth interview of 843 eligible cases, and review of those eligible cases reporting life-threatening complications by expert and lay panel.

This research is supported by the United States Agency for International Development, through PRIME and MotherCare.

**Does the hominid mandibular corpus have any taxonomic utility?** N. SILVERMAN, Doctoral Program in Hominid Paleobiology, B. RICHMOND, and B. WOOD, Department of Anthropology, The George Washington University, 2110 G St., NW, Washington, DC 20052.

Mandibular corpora, for taphonomic reasons, are well-represented in the hominid fossil record. However, the conventional wisdom is that the hominid mandibular corpus is a poor source of taxonomic information, but to our knowledge this proposition has not been formally tested. This study investigates whether linear measurements of the base of the corpus, and of the alveolar process, are able to discriminate between living hominid taxa. Discriminant function analysis was applied to raw data (ten linear measurements on the mandibular corpus), and size-adjusted data (each variable divided by the geometric mean) to assess their taxonomic utility in living hominids and fossil hominin taxa.

Two subspecies of *Gorilla* (N=48), two subspecies of *Pongo* (N=57), one subspecies of *Pan* (N=56), modern *Homo sapiens* (N=52), and four early hominin species, *Homo erectus* (N=4), *Homo ergaster* (N=2), *Australopithecus habilis* (N=2), and *Australopithecus rudolfensis* (N=2), were included in the analysis.

Using the raw data the fossil hominins were all correctly classified and were not confused with living taxa, and *vice versa*. For the size-adjusted data two *H. erectus* specimens were misallocated to *H. sapiens* and *A. habilis* but none of the other fossil mandibles were misallocated.

Mandibular corpus morphology (raw and size-adjusted) apparently can discriminate among *H. sapiens*, *P. troglodytes*, *G. gorilla*, and *P. pygmaeus*. In particular, *H. sapiens* and *P. troglodytes* are correctly classified 100% of the time using both the raw and size-adjusted data. Fossil hominin groups are correctly classified 80% of the time using the size-adjusted data or 100% using the raw data. These results suggest that the hominid mandibular corpus can provide taxonomic information, so that even within *Homo* it is possible to discriminate edentulous mandibular corpora at the species level.

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